

Figure S9 – Transcription Factor Binding for rs6311

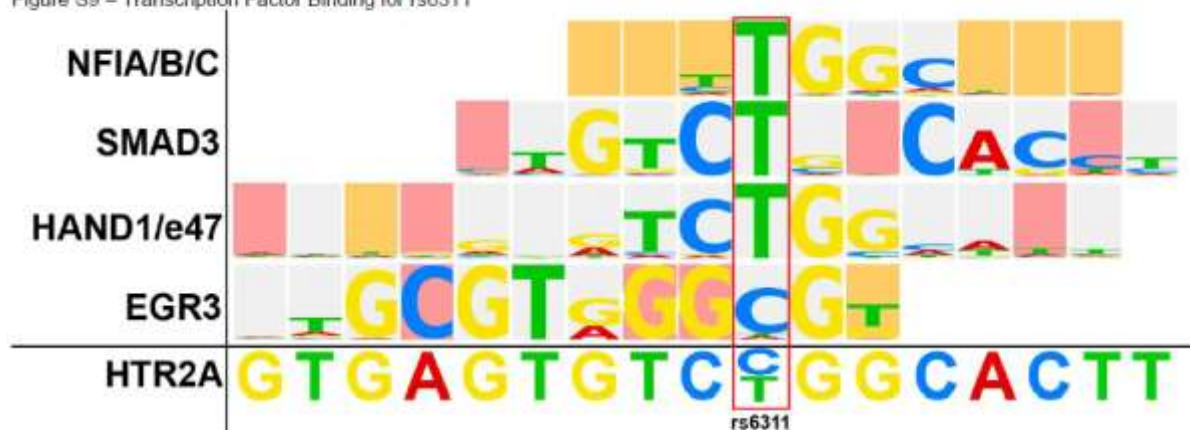


Figure S8. Transcription factor binding sites predicted for rs6311 alleles. The consensus *HTR2A* human reference sequence is represented on the bottom row, with the predicted transcription factor alignments above. The bi-allelic rs6311 position is denoted by the red box. Weak matches, where the second nucleotide in the transcription factor prediction weight matrix constitutes >20% of the total weight, are shaded orange, while mismatches (<20%) are shaded pink.